CONCLUSION

Changes have been made to the specification to reflect the renumbering of the Figures. No new matter has been added. Entry of the Preliminary Amendment is respectfully requested. If the Examiner feels that a telephone conference would expedite prosecution of this case, the Examiner is invited to call the undersigned at (978) 341-0036.

Respectfully submitted,

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MARKED UP VERSION OF AMENDMENTS

Specification Amendments Under 37 C.F.R. § 1.121(b)(1)(iii)

Replace the paragraph at page 5, line 20 with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

- - -[Fig. 1] Figs 1A and 1B show the results of fine mapping of chromosome 9. - - -

Replace the paragraph at page 5, lines 21-22, with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

- - - [Fig 2] Figs. 2A-2D show the results of an association study performed on 204 cases and 117 controls.- - -

Replace the paragraph at page 32, lines 6-13, with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

- - -An initial whole genome scan was performed on 167 individuals from 22 families. This allowed the identification of four chromosomal regions with NPL scores greater than 1.60. One of these peaks (NPL score = 2.35) was at D9S925. Using the GeneMap '98 (http://www.ncbi.nlm.nih.gov/genemap/), it was determined that the VLDLr gene locus was located within 23 cM of D9S925. In subsequent fine mapping of this region with 21 additional families and six additional markers from the region, the peak shifted to D9S285, and the NPL value increased to

2.79. This marker is estimated to be about 20 cM from the VLDLr locus [(Fig.1).] (Figs. 1A and 1B).- - -

Replace the paragraph at page 33, lines 5-12, with the below paragraph marked up by way of bracketing and underlining to show the changes relative to the previous version of the paragraph.

- - -In the Chicoutimi case-control cohort, the major alleles had repeat sizes of 5, 8 and 9, which accounted for 98% of all alleles. Minor alleles with repeat sizes of 7, 10 and 11 were seen in this population. In the association study, performed on 204 cases and 117 controls, it was determined that individuals who are homozygous for five repeats, the "5/5 genotype", have a reduced susceptibility to CHD (odds ratio of 0.55 at the 0.046 significance level) [(see Fig. 2).] (see Figs. 2A-2D). The case control study also found odds ratios of 1.45 and 1.60 for the 8/8 and the 8/9 genotypes, respectively, but neither of these results was statistically significant.- - -